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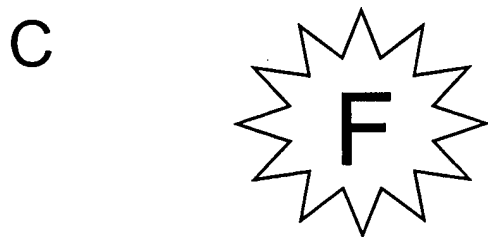
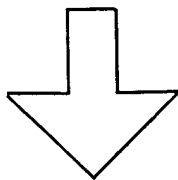
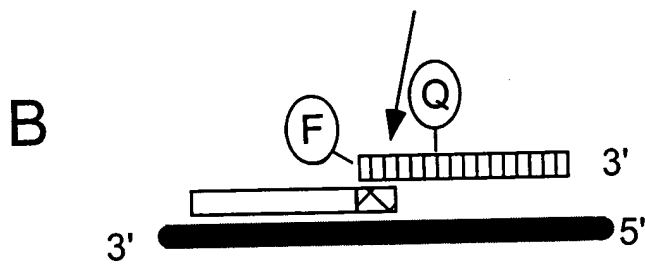
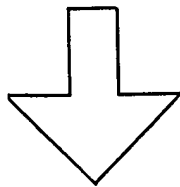
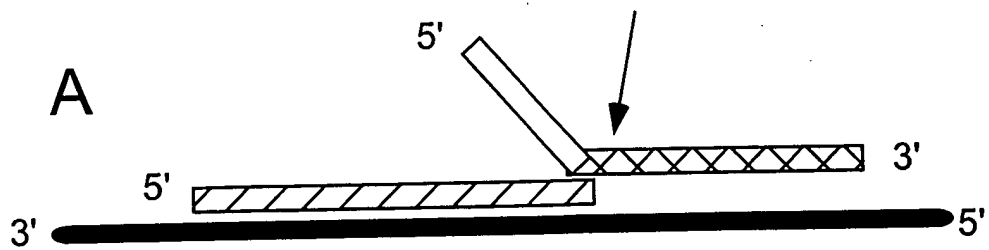


FIGURE 1

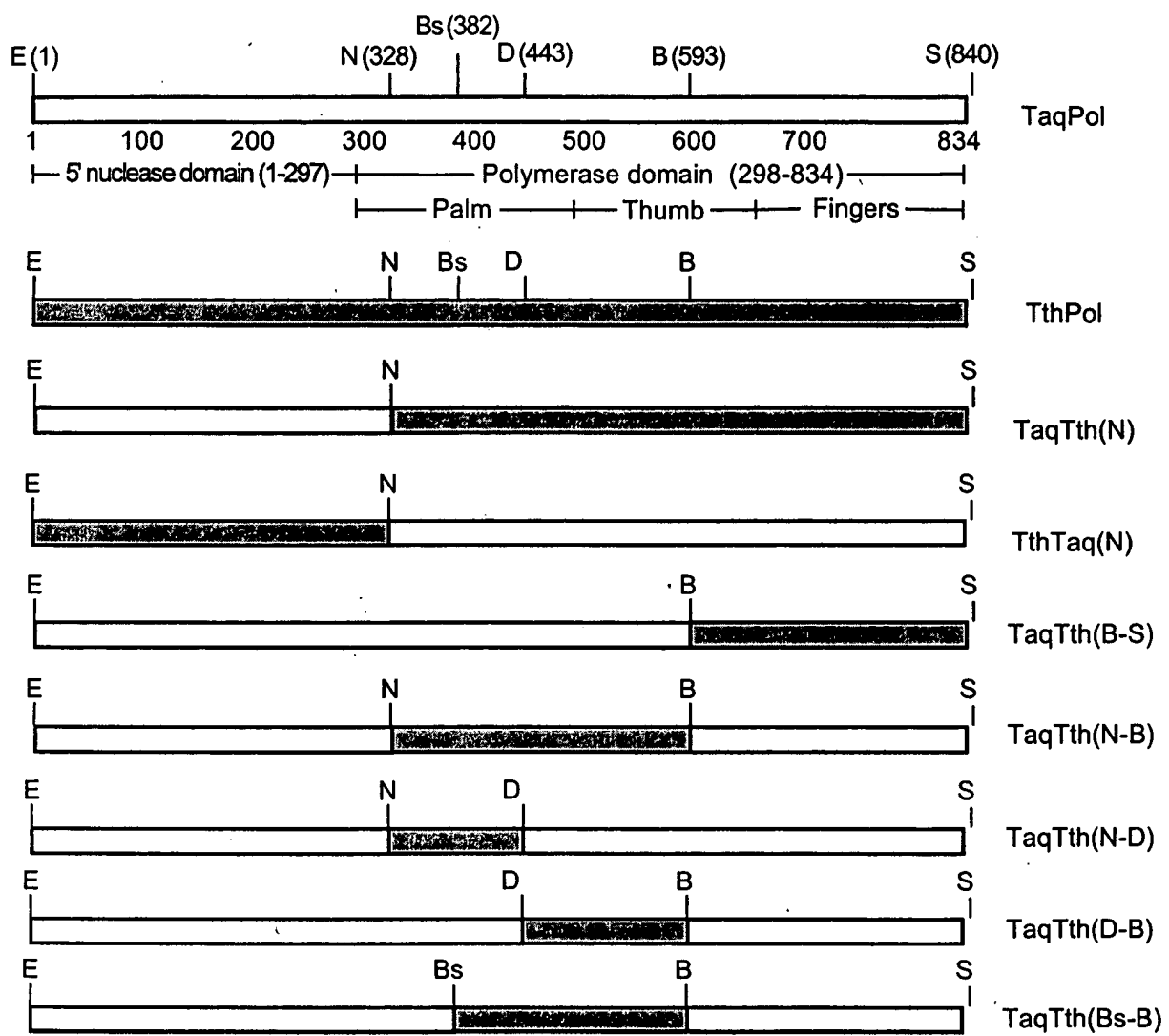


FIGURE 7

[illegible]



FIG. 8B

MAJORITY [SEQ ID NO:7]	CGAGCGGACGACGCTXCTGGCCACCCTGGCCCAAGAGGGCGAAAGGAGGGGTACGAGGTGGGGCATCGCTC	
DNAPTAO [SEQ ID NO:1]	.....C.....G.....C.....	417
DNAPTFL [SEQ ID NO:2]	T.....G.....CG.....	414
DNAPTTH [SEQ ID NO:3]	.....T..G.....	420
MAJORITY	ACGCGCGAGCGGACGCTCTACCAGCTCGTTTCGGACCGCATCGCGGTCCTCCACCCCGAGGGGTACCTCA	
DNAPTAO	.....AAA.....T.....CA.....	487
DNAPTFL	..T.....G..G.....A.....T.....G..	484
DNAPTTH	.....A..G.C.....G.....CC.....	490
MAJORITY	TCACCCCGCGGTGGCTTTGGGAGAAGTACGGCCCTGAGGGCCGGAGGAGTGGGTGGACTACCGGGGGCTGGC	
DNAPTAO	.....C.....A.....C..C.....CC.....A..	557
DNAPTFL	.....AC.....C.C.....	554
DNAPTTH	.....A.....C.....T..C.....C.T 560	
MAJORITY	GGGGGACCCCTCGGACACCTCCCGGGGTCAAGGGGTCAAGGGCATCGGGGAGAAAGACCGCCCGGAGGCTCCTCXAG	
DNAPTAO	C.....GAG.....T.....G..GAG.....T..GG..	627
DNAPTFL	.....G..T..A.....G.....A..G....A..CGC 624	
DNAPTTH	.....TC.....A..	630
MAJORITY	GAGTGGGGGAGGCTGGAAGACCTCCTCAAGAACCTGGACCGGGGTGAAGCCCGCC...CXTCCCGGAGAGA	
DNAPTAO	.....GC.....G.....A.....	694
DNAPTFL	.....T..C..C.....A.....T....T..G.....C 691	
DNAPTTH	.....A.....A.....A.AAAA.G.....	700

FIG. 8C

MAJORITY [SEQ ID NO:7] TCGAGGCCACATGGAXGACCTGAXGCTCTGCTGGGAGGCTXTCGCAGGTGGGACGGACCTGCCCGCTGGA  
DNAPTAO [SEQ ID NO:1] ...T...C..T...A...C..GG..A... 764  
DNAPTFL [SEQ ID NO:2] ...GGG...G.C...GCC.T...C..A...T...A..T... 761  
DNAPTTH [SEQ ID NO:3] ..A...C...A...C.G...T...C...G...C... 770

MAJORITY GGTGGACTTCGCCAAGXGGCGGAGCGCGGAGCGGGGCTTAGGGGCTTCTGGAGAGGCTGGAGTIT  
DNAPTAO ...AA... 834  
DNAPTFL ...GG.G.C.C.CACA..A..T...T..GC...T...T...C..T... 831  
DNAPTTH ...C...C..G... 840

MAJORITY GGCAGGCTCCTCCAGGAGTTCGGGCTTCCTGGAGGGGCGCGCAAGGCGCTGGAGGAGGCGCGGCTGGCGCGCGG  
DNAPTAO ...T...AA... 904  
DNAPTFL ...A...G...G...GCGA...T... 901  
DNAPTTH ...C...C...GCGC... 910

MAJORITY CGGAAGGGGCTTCGTGGGCTTGTGCTTTCGGGCGCGGAGGCGCAATGTGGGCGGAGGCTTCTGGCGGCTGGC  
DNAPTAO ...G...AAG...T... 974  
DNAPTFL ...T..T...TC.T...T... 971  
DNAPTTH ...C...C...G...AAA... 980

MAJORITY GCGCGGCGAGGGGCGGCTCCAGCGGGGACGACAGACCGCTTAXGGCGCTXAGCGGACCTXAAGGAGGTG  
DNAPTAO ...G...C..C..G..T.A..AA.C...C...G...C... 1044  
DNAPTFL T.GG..GT...G..CC...T...A...C...G...G...T...G... 1041  
DNAPTTH ...TG...C...G...GCG...G..A.A...C...C... 1050



FIG. 8E

MAJORITY [SEQ ID NO:7] GGAGATCCGCGCGCTCGAGAGGAGGTCTTCGCGCTGCGCGGCGACCCCTCAACCTCAACTCCCGGGGAC

DNAPTAQ [SEQ ID NO:1] .....CC..... 1464  
 DNAPTFL [SEQ ID NO:2] .....G.G....AG..G..... 1461  
 DNAPTTH [SEQ ID NO:3] .....T.....G..... 1470

MAJORITY CAGCTGGAAGGGTGCTCTTGACGAGCTXGGGCTTCCCGCCATCGGCAAGACGGAGAGACXGGCAAGC

DNAPTAQ .....C.....A..... 1534  
 DNAPTFL .....CC.....G..C..G..T.....G..G..A. 1531  
 DNAPTTH .....TA.....T.G..G.....C.A..... 1540

MAJORITY GCTCCACGAGCGCGCGTGCTGGAGGGCTXCGXGAGGCCCGCCATCGTGGAGAAGATCCTGCAGTA

DNAPTAQ .....C.....C..C..... 1604  
 DNAPTFL .....T.....G..A.....CGC..... 1601  
 DNAPTTH .....G.....A..G.....C...C. 1610

MAJORITY CCGGGAGCTCACCAGGCTCAAGAACACCTACATXGACCCCTGCCXGXCCTCGTGCACCCCGAGCGGGC

DNAPTAQ .....G....G.....T....T....G.A....A..... 1674  
 DNAPTFL .....A.....A.....C.C..G.....A...C... 1671  
 DNAPTTH .....G.G.....G.G.....C..AAG.....G..... 1680

MAJORITY CCGCTCCACACCGCGCTCAACCAGACGGGCCACGGCCAGCGGCGGCTTAGTAGCTCCGAGCCCAACCTGC

DNAPTAQ .....A.....T.....C. 1744  
 DNAPTFL .....G.....C.....TCC..... 1741  
 DNAPTTH .....G.....G..... 1750





FIG. 8F

MAJORITY	[SEQ ID NO:7]	AGAACATCGCGCGTGGGACGCGCCXCTGGGCCAGAGGATCGGCGCGGCCCTTCGTGCGCGAGGAGCGGXTGGGT	
DNAPTAQ	[SEQ ID NO:1]	.....G..T..G.....A..C.....G....C..	1814
DNAPTFL	[SEQ ID NO:2]	.....G.....T.....C..C.....A.....C.....C.....	1811
DNAPTTH	[SEQ ID NO:3]	.....CT.....C.....C.....T.....C.....T.....C..	1820
MAJORITY		GTGGTGGCCCTGGACTATAGCCAGATAGAGCTCCGGGTCTGGCCACCTCTCGGGGAGCGAGAACCTG	
DNAPTAQ		A.....T.....C.....A.....G.....C.....C.....	1884
DNAPTFL		.....T..T.....C.....T.....T.....C.....C.....	1881
DNAPTTH		.....C.....C.....C.....C.....A.....A.....	1890
MAJORITY		ATCGGGGTCTTCCAGGAGGGGAGACATCCACAGCCAGAGCGCCAGCTGGATGTTGGGGGTCCCCCGCG	
DNAPTAQ		.....C.....C.....GG.....G.....G.....G..	1954
DNAPTFL		.....T.....T.....T.....T.....T.....T.....C..	1951
DNAPTTH		.....A.....A.....A.....A.....A.....A.....	1960
MAJORITY		AGGCGGTGGACCCCTGATCGCGCGGGGGCCCAAGACCATCAACTTCGGGGTCCTCTACGGGCATGTCCGC	
DNAPTAQ		.....A..G..A.....T.....G.....G.....G..	2024
DNAPTFL		.....G.....G.....G.....G.....G.....G.....	2021
DNAPTTH		.....G.....G.....G.....G.....G.....G.....	2030
MAJORITY		CCACCGCCTCTCCAGGAGCTTCCCATCCCTACGAGGAGCGGGTGGCCCTCATTGAGCGCTAGTCCAG	
DNAPTAQ		.....A.....A.....T.....CCA.....T.....T...	2094
DNAPTFL		.....GG.....T.....T.....T.....T.....T...	2091
DNAPTTH		....TA.G.....T.....T.....T.....T.....A..	2100



FIG. 8G

MAJORITY [SEQ ID NO:7]	AGCTTCCCCAAGGTGGGGCCCTGGATTGAGAAGAGCCCTGGAGGAGGGCCAGGAGGGGGGTACGTGGAGA	
DNAPTAO [SEQ ID NO:1]	.....	2164
DNAPTFL [SEQ ID NO:2]	...A.....GG.....C.....C.CC.....T.....	2161
DNAPTTH [SEQ ID NO:3]	.....A.A.....G.....A.....C.....A.	2170
MAJORITY	CCCTCTTGGGGCCGGGGCTACGTGCCCGACCTGAACGGCGGGGTGAAGAGCGTGGGGGAGGGGGCGGA	
DNAPTAO	.....C.....A.....AG.G.....C.....	2234
DNAPTFL	.....T.....G.....G.....	2231
DNAPTTH	...AA.AA.....CA.....G.....	2240
MAJORITY	GGGCATGGCCCTTCAACATGCCCGCTCCAGGGCAGCGGGCGCGACCTCATGAAGCTGGCCCATGGTGAAGCTG	
DNAPTAO	.....	2304
DNAPTFL	.....G.....T.....CG...T	2301
DNAPTTH	.....C.....G.....	2310
MAJORITY	TTCCCGGGCTXCAGGAAATGGGGCCAGGATGCTGCTXCAGGTCACAGCAGGAGCTGCTCCTGGAGGGCC	
DNAPTAO	.....A...GG.....T.....	2374
DNAPTFL	.....T...G.....TT.G.....G.....	2371
DNAPTTH	.....C.C.G...G.....C.C.....CC...G.....	2380
MAJORITY	CCAAAGAGCGGGGGAGGXGGTGGCCGGCTTGGCCCAAGCAGGTCATGGAGGGGGGTCTATCCCCCTGGCCGT	
DNAPTAO	.....A.....CC.....CGGC.....G.....	2444
DNAPTFL	.....G.C.....AG...A.....CC.....CAG...	2441
DNAPTTH	.....C...C.....A.....G.....AA..C.....C.....	2450

FIG. 8H

MAJORITY [SEQ ID NO:7] GCGCGCTGGAGGCTGGCGCATGGGGGAGGACTGGCTCTCCGCCCAAGGAGTAG

DNAPTAA [SEQ ID NO:1]

DNAPTFL [SEQ ID NO:2]

DNAPTTH [SEQ ID NO:3]

.....A.....GA  
.....CC.....  
.....T.....GT...

2499

2496

2505





FIG. 9A

MAJORITY [SEQ ID NO: 8] MXAML PLFEPKGRVLLVDGHHLAYRTFFALKGLTTSRGEVPQAVYGFAKSLKALKEDG- DAVXVVVFDK

TAO PRO [SEQ ID NO: 4] . RG. .... H. .... I. .... 69  
TFL PRO [SEQ ID NO: 5] . . . . . V. V. .... 68  
TTH PRO [SEQ ID NO: 6] . E. .... YK. F. .... 70

MAJORITY APSFRHEAYEAYKAGRPTPEDFPROLALI KELVDLLGLXRLEVPGEADDVLATLAKKAEKEGYEVRI L

TAO PRO . . . . . GG. .... A. .... S. .... 139  
TFL PRO . . . . . V. .... F. .... R. .... 138  
TTH PRO . . . . . FT. .... . .... 140

MAJORITY TADRDLYQLSDRI AVLHPEGYLI TPWLWEKYGLRPEQWVDYRALXGDPDSNLPGVKGI GEKTAXKLLX

TAO PRO . . . . . K. .... H. .... D. A. . . . . T. E. .... R. . . . . E 209  
TFL PRO . . . . . E. I. .... Y. .... A. . . . . I. .... OR. I R 208  
TTH PRO . . . . . V. V. .... H. E. .... F. V. .... L. . . . . K 210

MAJORITY EWGSLENLLKNLDRVKP- XXREKI XAHME DLXLSXXLSXVRTDLPLEVDFAXRREPDRGLRAFLELRF

TAO PRO . . . . . A. .... L. . . . . AI. . . . . L. . . . . D. K. . . . . WD. AK. .... K. .... R. .... 278  
TFL PRO . . . . . FOH. O. . . . . SL. . . . . LQ. G. . . . . A. A. . . . . RK. O. H. .... GR. T. NL. .... 277  
TTH PRO . . . . . ENV. . . . . K. L. . . . . R. LE. R. .... L. OG. .... . .... 280

MAJORITY GSLLHEFGLLEXPKALEEAPWPPPEGAFVGFVLSRPEPMWAE LLALAAARXGRVHRAXDPLXGLRDLKEV

TAO PRO . . . . . S. .... . . . . K. .... D. .... G. .... PE. YKA. .... A 348  
TFL PRO . . . . . G. A. .... L. SF. .... G. WE. L. O. R. .... G. 347  
TTH PRO . . . . . A. AP. .... . . . . K. C. D. .... A. A. K. .... 350



FIG. 9B

MAJORITY [SEQ ID NO: 8] RGLLAKDLAVLALREGLDXPGDDPML LAYLLDPSNTTPEGVARRYGGEWTE DAGERALLSERLFXNLXX

TAO PRO [SEQ ID NO: 4] ..... S ..... G. P ..... E ..... A ..... A ..... WG 418  
TFL PRO [SEQ ID NO: 5] ..... I ..... F. E ..... A ..... QT. KE 417  
TTH PRO [SEQ ID NO: 6] ..... S ..... V ..... AH ..... HR. LK 420

MAJORITY RLEGEERLLWLXYEVEKPLSRVLAHMEATGVRLDVAYLOALSLEVAEEI RRLEEEVFRLAGHPFNLNSRD

TAO PRO ..... R. R. A. R. A. A. 488  
TFL PRO ..... K. E. R. EA. V. O. 487  
TTH PRO ..... K. H. L. 490

MAJORITY QLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPI VEKILOYRELT KLKNTYI DPLPXLVHPRTG

TAO PRO ..... S. D. I. 558  
TFL PRO ..... DR. A. K. 557  
TTH PRO ..... R. L. O. H. V. S. 560

MAJORITY RLHTRFNQTATATGRLLSSSDPNLONI PVRTPLGORI RRAFVAEEGWXLVALDYSQI ELRVLAHLSGDENL

TAO PRO ..... I. L. 628  
TFL PRO ..... V. V. 627  
TTH PRO ..... A. A. 630

MAJORITY I RVFOEGRDI HTOTASWMF GVPPEAVDPL MRRAAKTI NFGVLYGMSAHRLSOELAI PYEEAVAFIERYFO

TAO PRO ..... E. R. O. 698  
TFL PRO ..... S. G. G. S. 697  
TTH PRO ..... K. V. 700

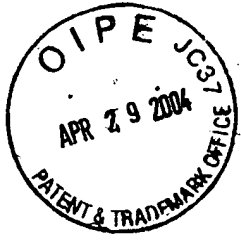


FIG. 9C

MAJORITY [SEQ ID NO:8]		SFPKVRAWI EKTLEEGRRRGYVETLFGRRRYVPDLNARVKSUREAAERMAFNMPVOGTAADLMKLMVKL	
TAO PRO [SEQ ID NO:4]		.....E.....	768
TFL PRO [SEQ ID NO:5]		Y.....G.....	767
TTH PRO [SEQ ID NO:6]		.....K.....	770
MAJORITY		FRLXEMGARMLOVHDELVL EAPKXRAEXVAALAKEVMEGVYPLAVPLEVEVGXGEDWLSAKEX	
TAO PRO		.....E.....E...A...R.....I.....	833
TFL PRO		.....O.L.....D...R.....W..O.....L.....	831
TTH PRO		.....R.....L.....OA...E.....A...KA.....M.....G	835

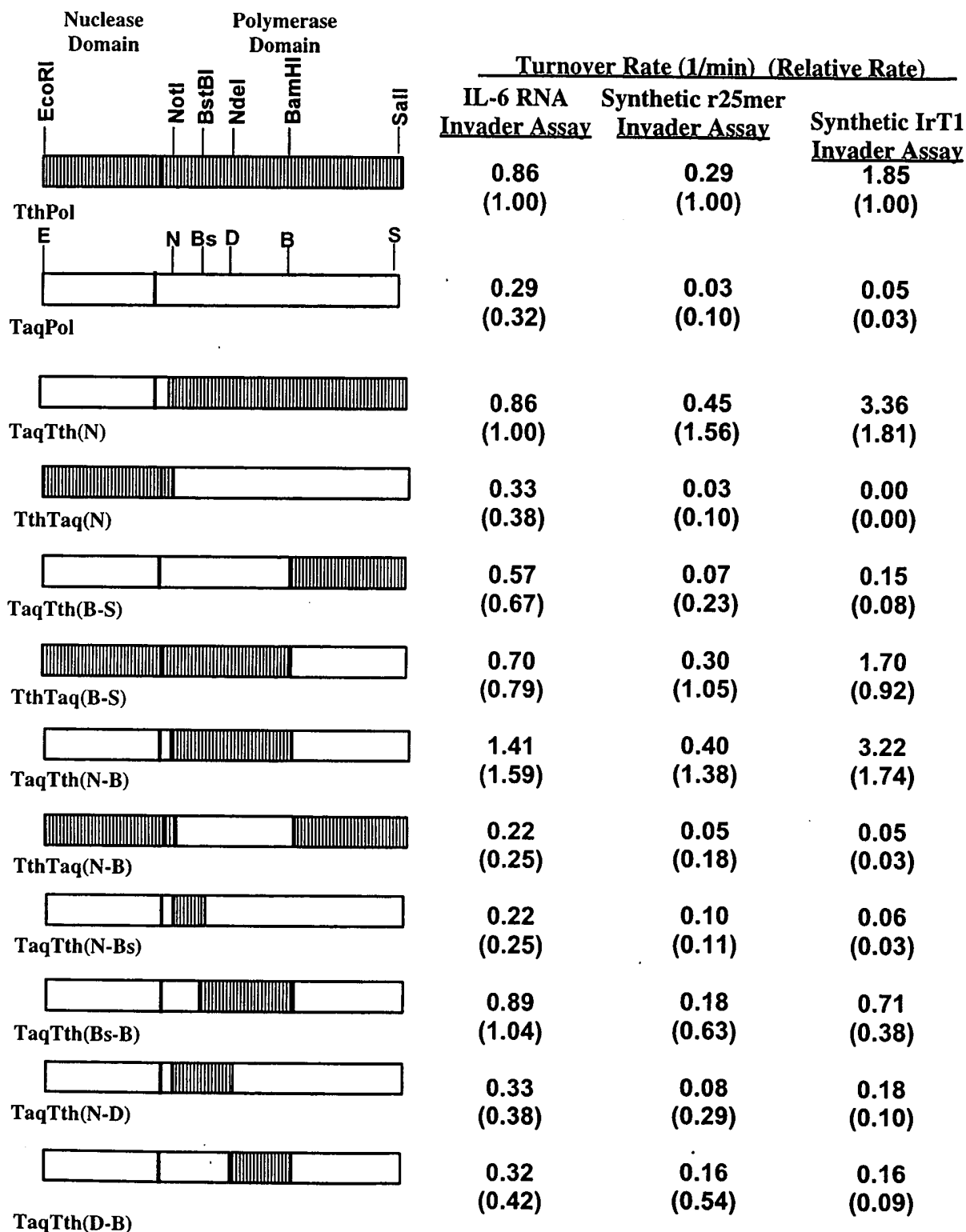


FIGURE 19

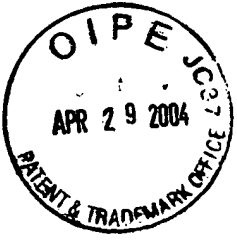


FIGURE 25

